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Figure 1

1 agatcatgcatcggttgagccgcttggtggg
 31 cgagacgggctcgatgggctccccgagcgggcacgcgggctcgatgaagtactcc
 85 ccgtgcttcacttctgcgccacgggtgatctccttgggtcgggtccaagccgaaa
 139 cctagctccggggacctcccctcgcccgccgggagctcgcccgaagaagccctac
 193 cccgcggatcgacgcgtcgccgcgtcgccggcgccggcgagggtacaaggcc
 247 atgtcccccgcgcggtgcccagatctcgccgagtgctcctcaccatccccgcc
 M S P A R L P I S R E S C L T I P A 18
 301 ggcttcagccccctcagcgctcctcgactcccccggtgctcctcaccaacttcaag
 G F S P S A L L D S P V L L T N F K 36
 355 gttgaaccttcaccaacaactggtagtctgggcatggctgagattctgcacaag
 V E P S P T T G S L G M A A I L H K 54
 409 agcgctcatccagacatgctgccttcgccacgggataaatctgttcgtaatgcc
 S A H P D M L P S P R D K S V R N A 72
 463 catgaagataggggttctagggattttgaattcaagcctcatctgaattcgtct
 H E D R G S R D F E F K P H L N S S 90
 517 tctcaatcactggctcctgctatgagtgatctaaaaaaacatgagcattctatg
 S Q S L A P A M S D L K K H E H S M 108
 571 caaaatcagagtatgaatcccagctcatctcatctagcaaatatggtgaataaac
 Q N Q S M N P S S S S S N M V N E N 126
 625 agacctccctgttcacgtgagtcgagcttaccagtgaaatgtaagtgtcagaac
 R P P C P R E S S L T V N V S A Q N 144
 679 caacctgttggaatgggttggttgactgacagcatgcctgctgaagttggtaca
 Q P V G M V G L T D S M P A E V G T 162
 733 tctgagccgcagcagatgaatagctctgacaatgccatgcaagagccgcagctct
 S E P Q Q M N S S D N A M Q E P Q S 180
 787 gaaaatgttgctgacaagtcggcagatgatggctacaactggcggaataacggg
 E N V A D K S A D D G Y N W R K Y G 198
 841 cagaagcatgtcaagggaagtgaaccctagaagttactacaagtgacacat
 Q K H V K G S E N P R S Y Y K C T H 216
 895 cctaattgtgaagtaaaaaagctattggagcgtgcagttgatggctgtgatcacg
 P N C E V K K L L E R A V D G L I T 234
 949 gaagttgtctataagggacgccacaatcctcctaagccccagccccaataggag
 E V V Y K G R H N H P K P Q P N R R 252
 1003 ttgctgggtggtgagttccttcaaacagggtgaagaacgatatgacggcgcgt
 L A G G A V E S N Q G E E R Y D G A 270
 1057 tcagctgctgatgataaatcttccaatgctcttagcaaccttgctaattccggta
 S A A D D K S S N A L S N L A N P V 288
 1111 cattcgccctggatgggttgagcctgttcagcttcagttagtgatgatgacatc
 H S P G M V E P V P A S V S D D I 306
 1165 gatgctggaggtggaagaccctaccctggggatgatgctactgaggaggaggat
 D A G G G R P Y P G D D A T E E D 324
 1219 ttagagtcgaaacgcaggaaatggagtcgtggtattgatgctgctgatg
 L E S K R R K M E S A G I D A A L M 342
 1273 ggtaaacctaaccgtgagccccgtgtcgttcctcaaactgtaagtgaagttgac
 G K P N R E P R V V V Q T V S E V D 360
 1327 atcttggtgatgatggctatcggttgccggaatatggacagaaagttgtcaaagga
 I L D D G Y R W R K Y G Q K V V K G 378
 1381 aaccccaatccacggagttactacaatatgcacaagcacaggatgccctgtgagg
 N P N P R S Y Y K C T S T G C P V R 396
 1435 aagcatgttgagagagcatcacacgatcctaaatcagtgataacaacgtatgaa
 K H A V E R A S H D P K S V I T T Y E 414
 1489 ggaaaacataaccatgaagtccctgctgaggaatgcaaccatgagatgtcc
 G K H N H E V P A A R N A T H E M S 432
 1543 gcgcctcccataagaacgtgctgcatcagattaacagcaatatgccagcagc
 A P P M P N V V H Q I N S N M P S S 450
 1597 attggtggcatgatgagggcatgtgaagccaggaactacaccaaccaatattct
 I G G G M M R A C E A R N Y T N Q Y S 468
 1651 caggcggctgaaaccgacactgtcagtccttgatcttggtgttggaatcagccca
 Q A A E T D T V S L D L G V G I S P 486
 1705 aaccacagcgcgacgcgacaaaccaaatagcagtcctcaggtcctgaccagatgcag
 N H S D A T N Q M Q S S G P D Q M Q 504
 1759 tatcaaatagcaaacatgggttcgatgtacggcaacatgagacatccatcatca
 Y Q M Q T M G S M Y G N M R H P S S 522
 1813 atggcagcgcgcgggtacaaggaactctgctgcccgcagtgatggttcgaga
 M A A V Q G N S A A R M Y G S R 540
 1867 gaagagaaaggtaacgaagggtttactttcagagocacaccgatggaccattca
 E E K G N E G F T F R A T P M D H S 558
 1921 gctaacctatgctatagcagtgctgggaacttggtcatgggtccatgagaggga
 A N L C Y S S A G N L V M G P * 573
 1975 atgagagtgctctgcaaatgctcatagctccatgaatcatatattaccaacaatg
 2029 ctttgtaatgacaatctcttcagcaagattctcaattgtctcaattgtgtatcg
 2083 gttacaagtcagttcagccggaggcaagtatgctagtataagctatactgtggg
 2137 gcactgcagcaaaatacgcagtgctgtcttttaagtgcggaaaaggccctgtgtg
 2191 atgtagcatcgacgccctacattcgttgtagcagcgaacctaatatgattaatta
 2245 attagattatgagaatttggtttcgtgaactgtctaattcttctgtactggaata
 2299 ttgatagaaatatagattatggtaattttctttaaaaaaaaaaaaaaaaaaaaaaa
 2353 aa

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Figure 2

L. b. Sfr1HAASSTGIDAPKASASFFTS.....XASFNSTFLD.....LAKDADGEGS	43
L. b. hyy	MGCTPDNRVALGSGWQTFGSPFKEPTFSLLDGDOGGLSPDGHETS-CHLASGFEQGVN	44
L. b. hyy	MGCTPDNRVALGSGWQTFGSPFKEPTFSLLDGDOGGLSPDGHETS-CHLASGFEQGVN	45
L. c. wacky	MGCTPDNRVALGSGWQTFGSPFKEPTFSLLDGDOGGLSPDGHETS-CHLASGFEQGVN	46
L. c. Sfr1	MGCTPDNRVALGSGWQTFGSPFKEPTFSLLDGDOGGLSPDGHETS-CHLASGFEQGVN	47
A. c. unk	48
A. c. d-i	49
A. c. hyy	50
A. c. wacky20	51
A. v. GSR1283	52

[illegible][illegible]

1.	b.	SPF1	FNVE	-----	WQHAQGVQD	-----	DEKFTVQ	YUNNS	-----	QVQ	-----	Q
2.	a.	hsp	GDON	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
3.	e.	hsp	GDON	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
4.	e.	wyk	QLES	-----	RLWNGQDGVQD	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
5.	a.	hsp	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
6.	a.	unk	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
7.	a.	d-1	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
8.	a.	d-1	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
9.	a.	bvp	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
10.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
11.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
12.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
13.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
14.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
15.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
16.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
17.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
18.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
19.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
20.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
21.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
22.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
23.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
24.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
25.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
26.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
27.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
28.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
29.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
30.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
31.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
32.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
33.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
34.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
35.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
36.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FGCTG	SHG
37.	a.	hydro	QVH	-----	RLALGQDITK	-----	SLIS	-----	SLIS	-----	FG	

[illegible]

I. b.	SPFL	-----GTSRSTGRCGCT	-----SSTLR	-----GSGD
L. d.	bfp	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	bfp	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	bfp	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	wcky	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	ant	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	uok	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	d	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	bfp	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	bfp	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	wcky20	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG
L. e.	SPST02	KVVELSRKSTGTCGCGGSEFELF	-----DQSLDQ	AGCGGFVYAGAG

[illegible][illegible][illegible][illegible][illegible]

L. b. <i>sfpi</i>	-----ENNAAAAGCAIAPG-----PITPTTPTGCG	
L. b. <i>hnp</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	495
L. o. <i>hnp</i>	-----TCAATATGAGGCTG-----GCTCTGCGGCTG	637
L. t. <i>wcky</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	634
A. t. <i>gat</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	421
A. t. <i>wck</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	421
A. t. <i>d-i</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	421
A. t. <i>hnp</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	421
A. t. <i>wcky20</i>	-----TCAATATGAGGCTG-----GAAAGATGCTG	493

[illegible]

L. a.	h.	hpf	ROD	Left	Right	549
L. a.	h.	hpf	KVPL5DP	GPATQOP	NGLSLGHOM	729
L. a.	h.	hpf	KVPL5DP	GPATQOP	NGLSLGHOM	729
L. t.	w.	wky	KAPPHGDPGLSLHSGSITQOP	NGLSLGHOM	729	
L. t.	g.	gnt	KAPPHGDPGLSLHSGSITQOP	NGLSLGHOM	729	
L. t.	w.	wk	-----	NGLSLGHOM	485	
L. c.	d.	d-1	-----	NGLSLGHOM	485	
L. t.	h.	hpf	-----	NGLSLGHOM	485	
A. t.	w.	wky20	-----	NGLSLGHOM	571	

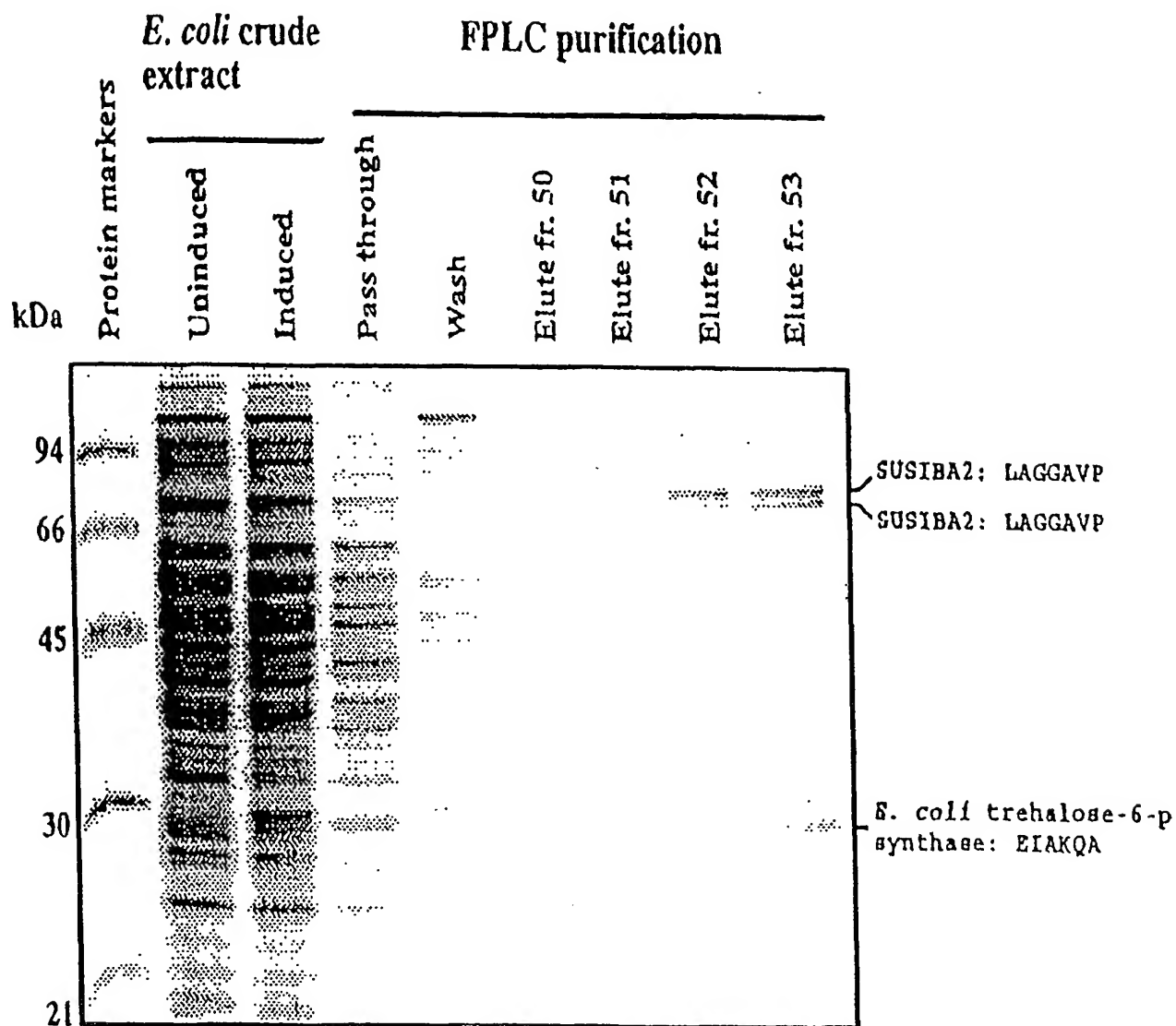
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Red

Pink

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Figure 3

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Figure 4**A**

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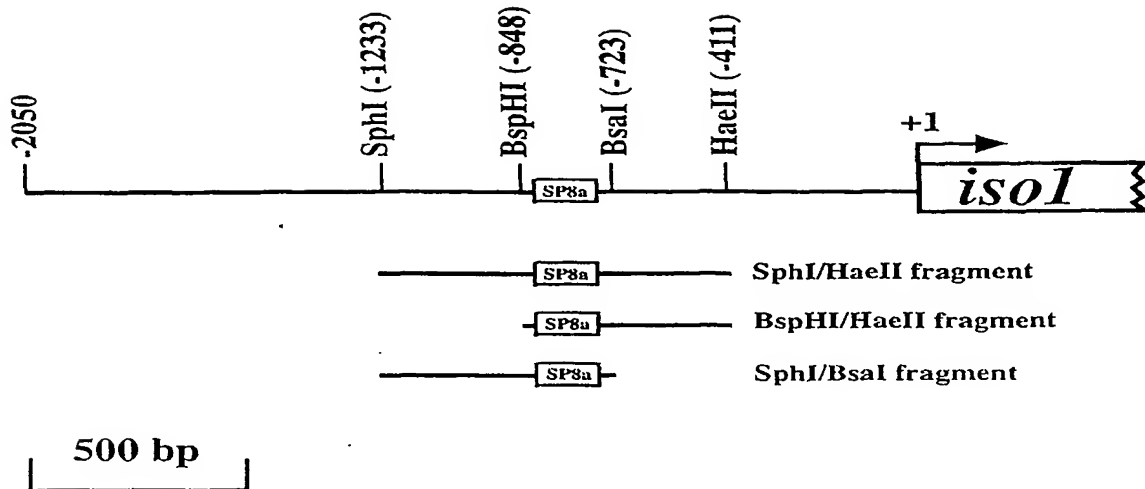
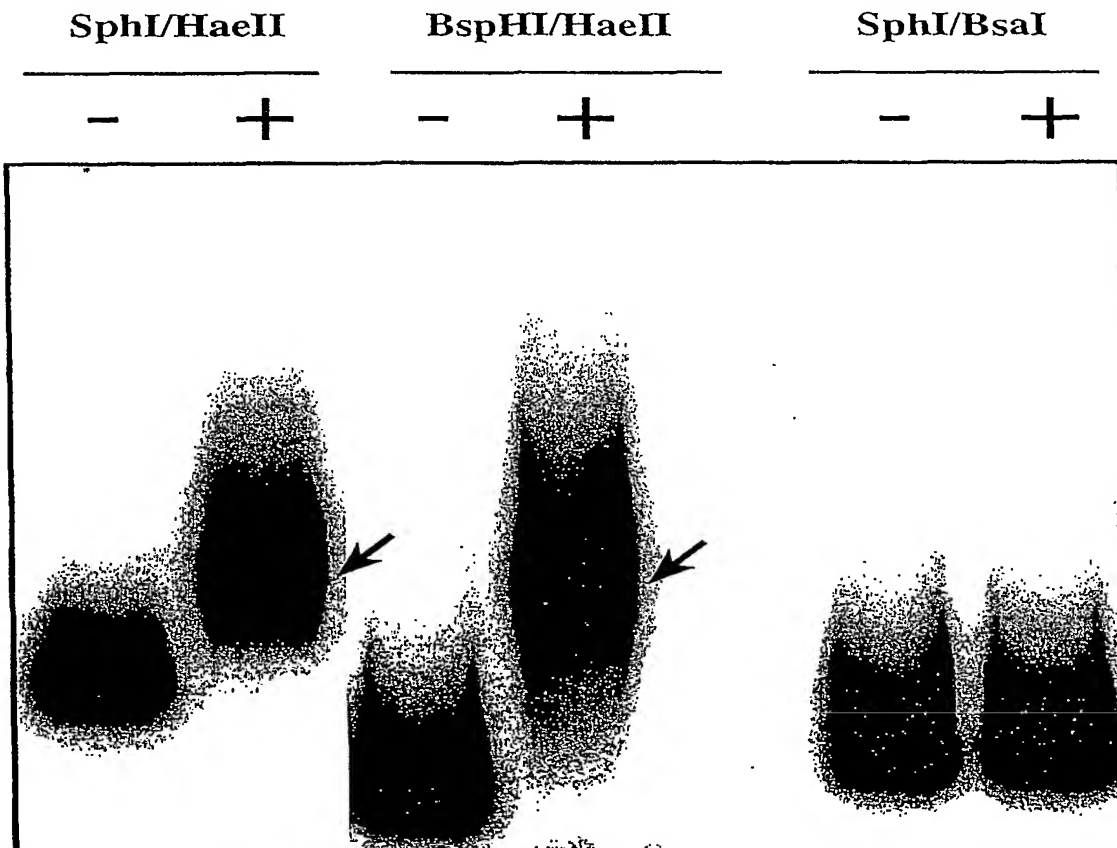
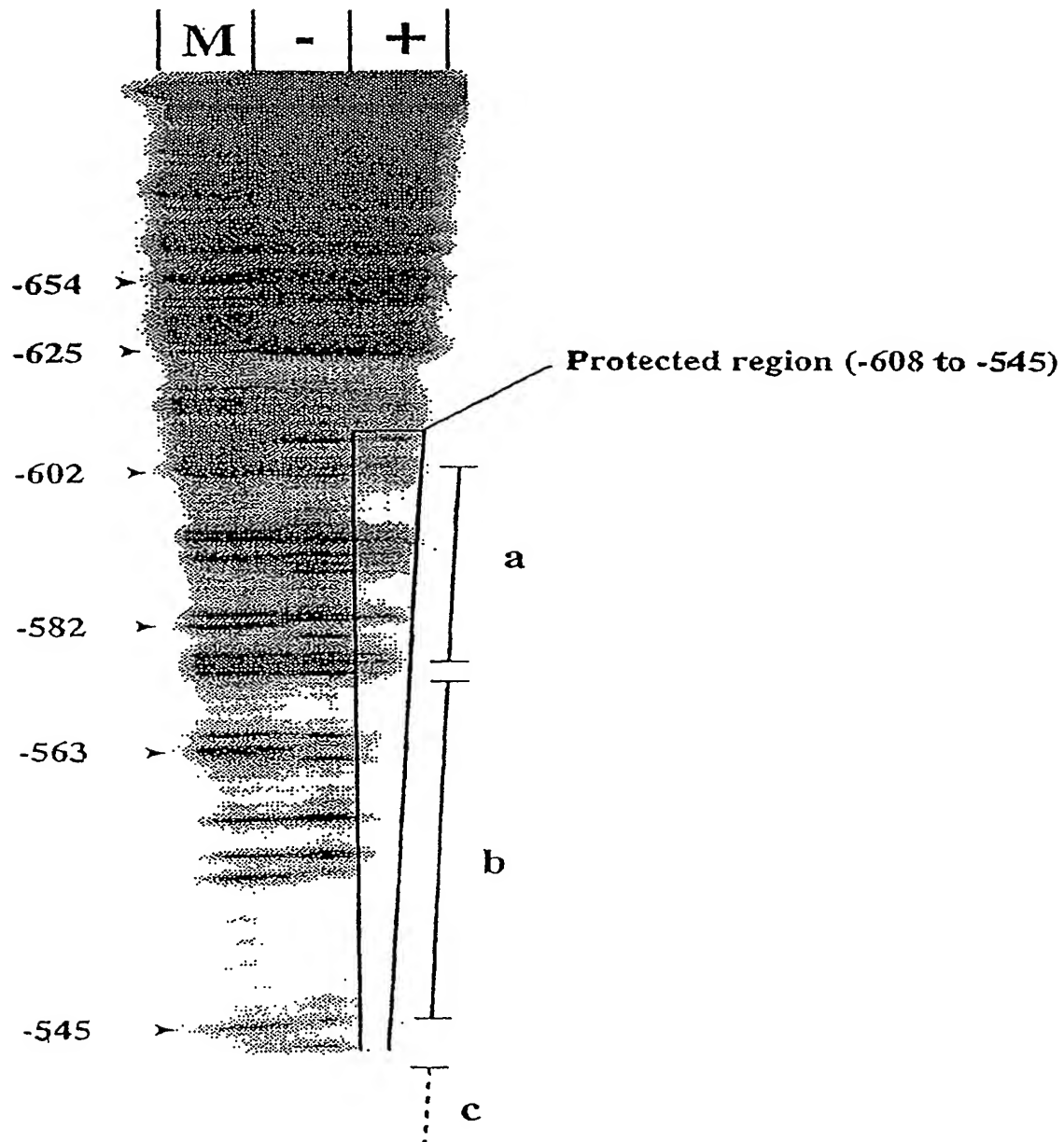
**B**

Figure 5

**B**

Patatin SURE sequence

|||||
AATACTAATAAAGA---ATAGAAAA

Patatin SURE sequence

||||| || ||| |||| ||||
AATACTAATAAAGAATAGAAAAA

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Figure 6

A

SP8a probe -772 CCCTCGTGGAAGCAAAACTGTGTTTCTCGC -743
GGGAGCACCTTCGTTTTGACACAAAGAGCG

SURE probe -578 GGAAAACCGAAATACCAAAAAATAATAATAAAATAATAAT -539
CCTTTTGGCTTTATGGTTTTTTATTATTATTTTATTATTA

W box probe -411 TCGCTAACCAGTGACTTCCACGTTTCATCATTTATT -376
AGCGATTGGTCACTGAAGGTGCAAAGTAGTAAATAA

B

SP8a

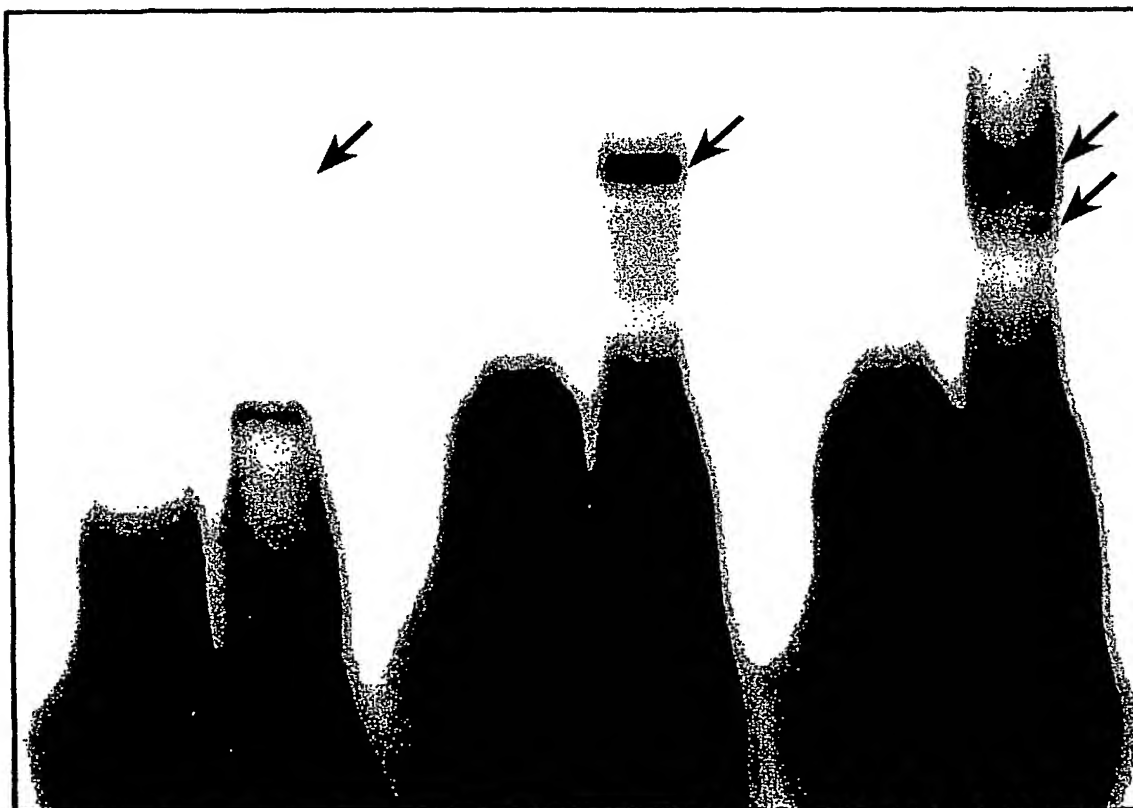
- +

SURE

- +

W box

- +

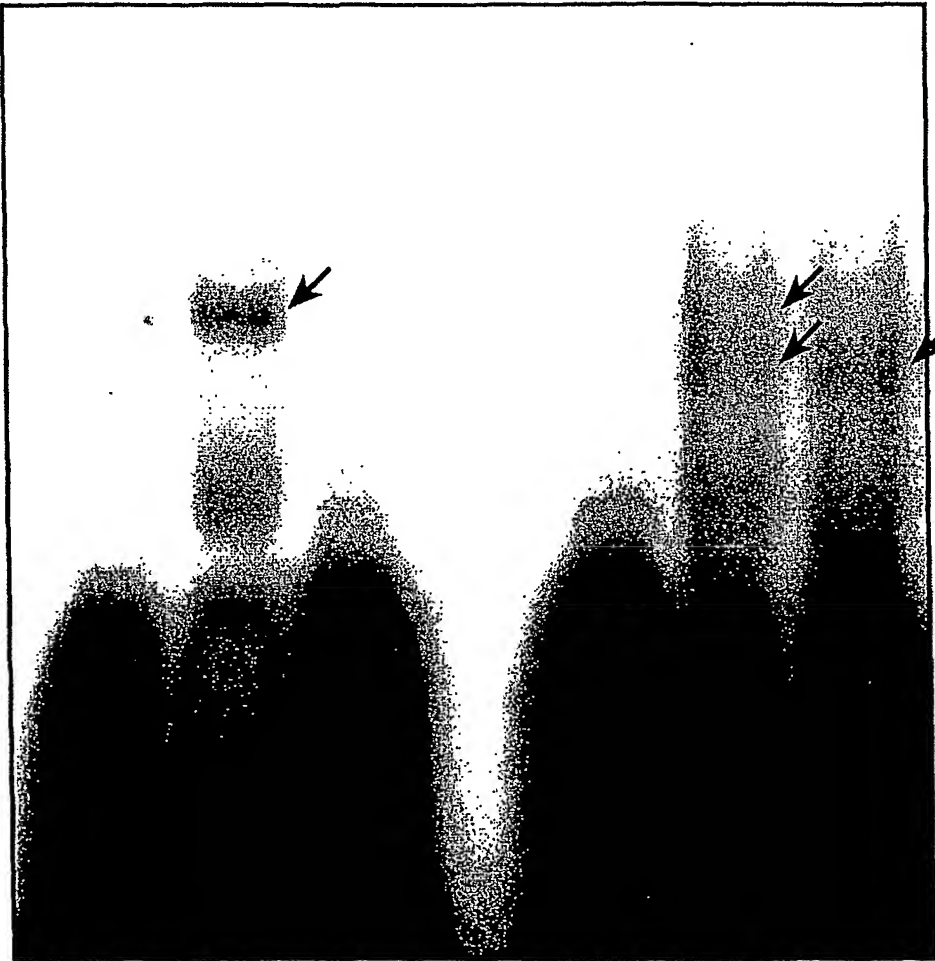


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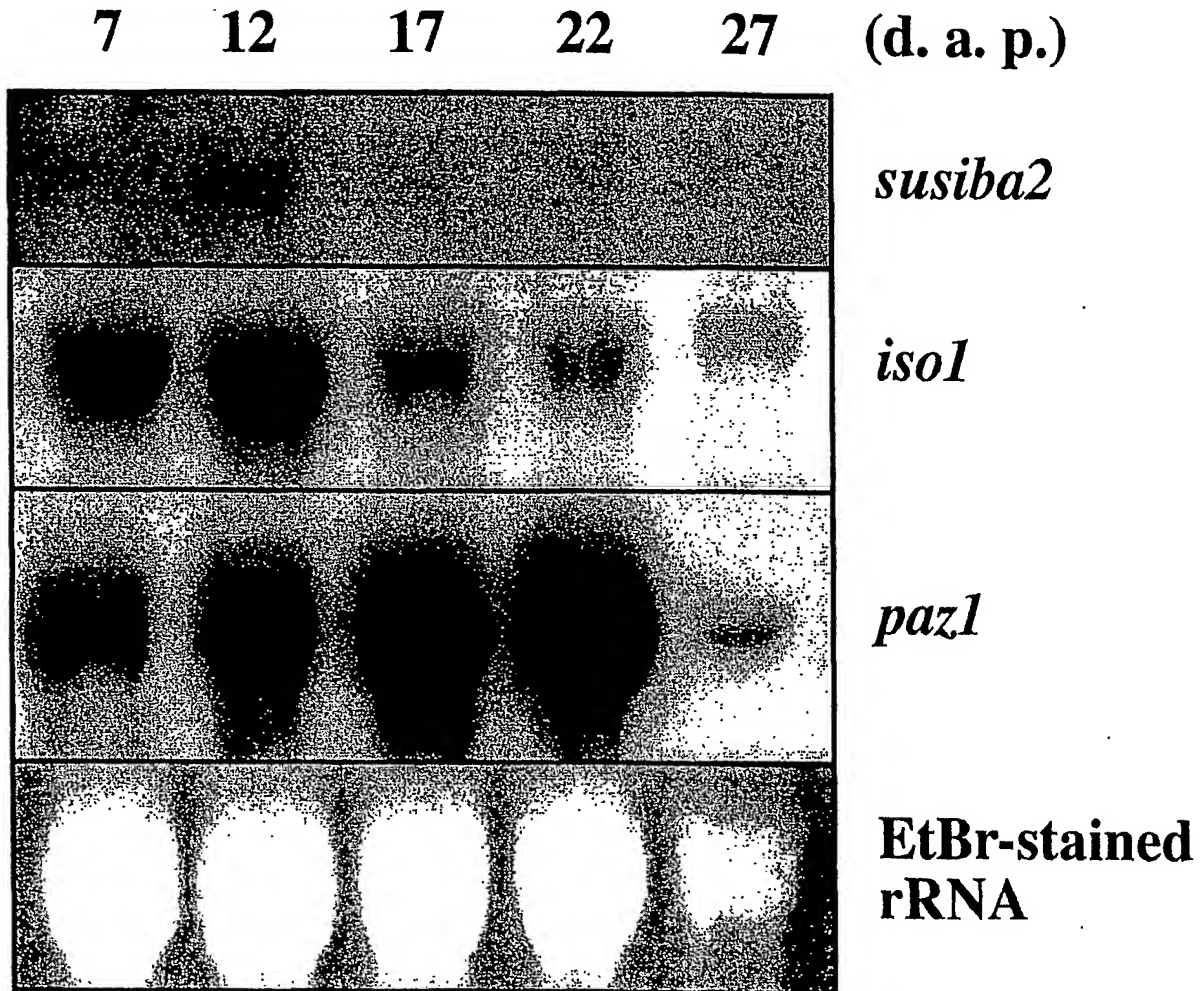
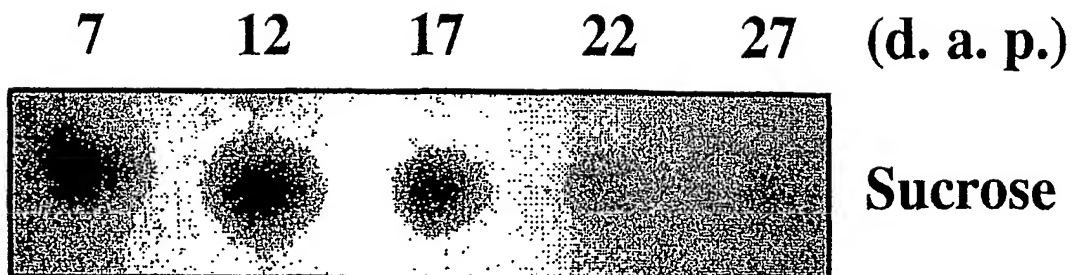
Figure 7

Probe:	SURE			W box		
Competitor:	-	-	W box	-	-	SURE
SUSIBA2:	-	+	+	-	+	+

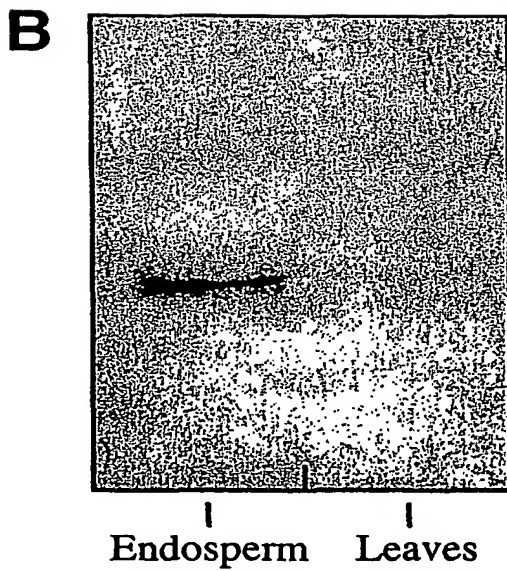
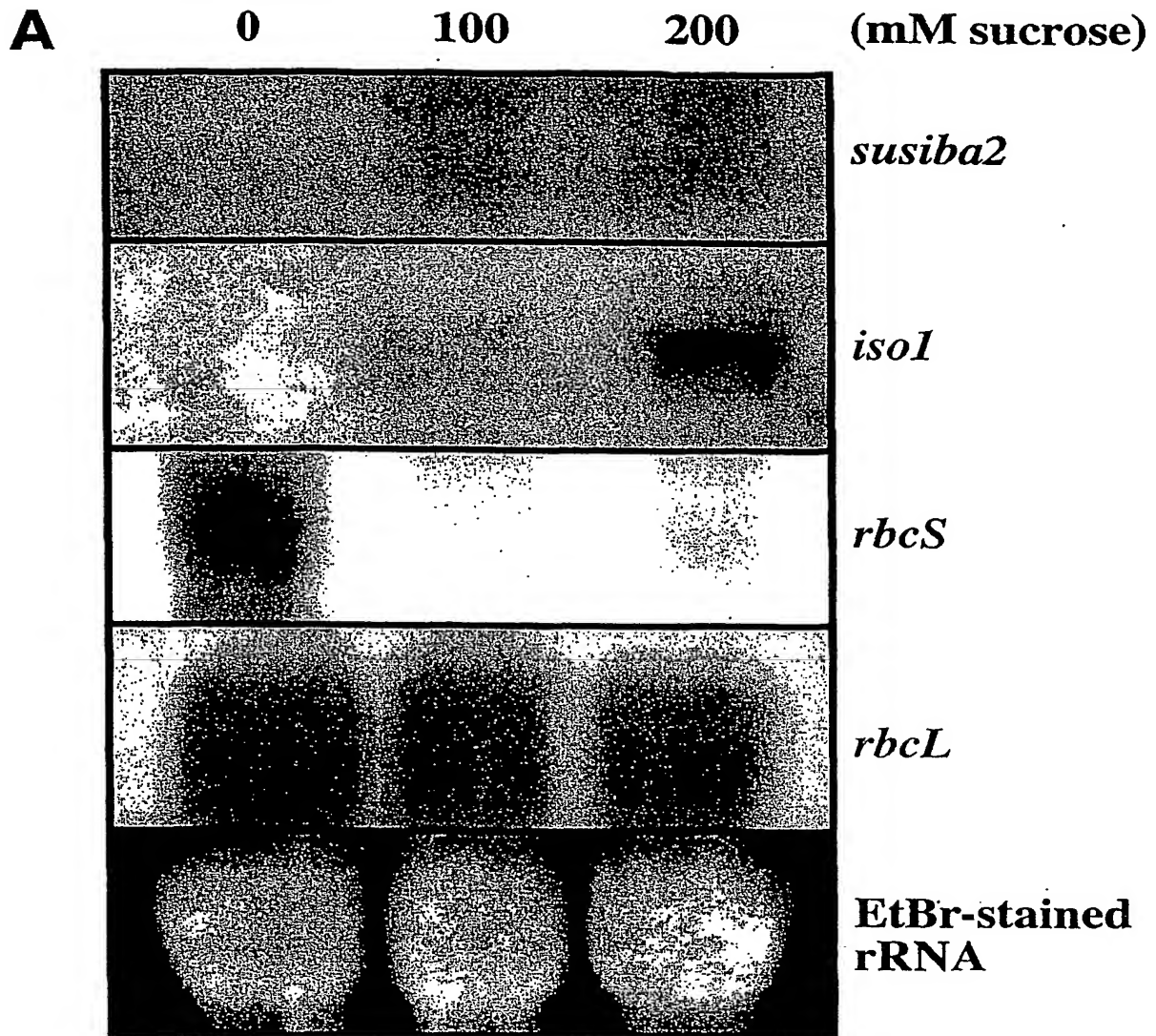


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Figure 8**A****B**

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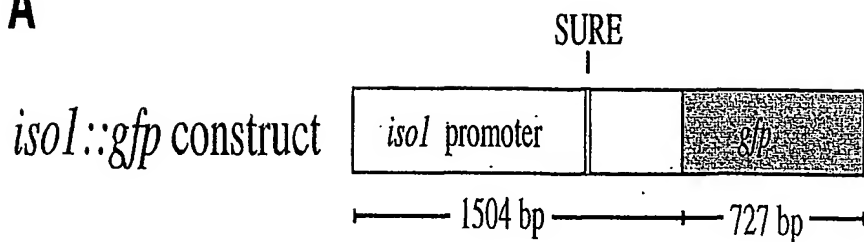
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Figure 9

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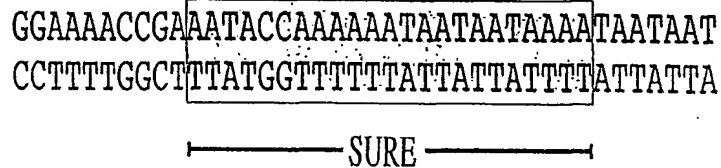
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Figure 10

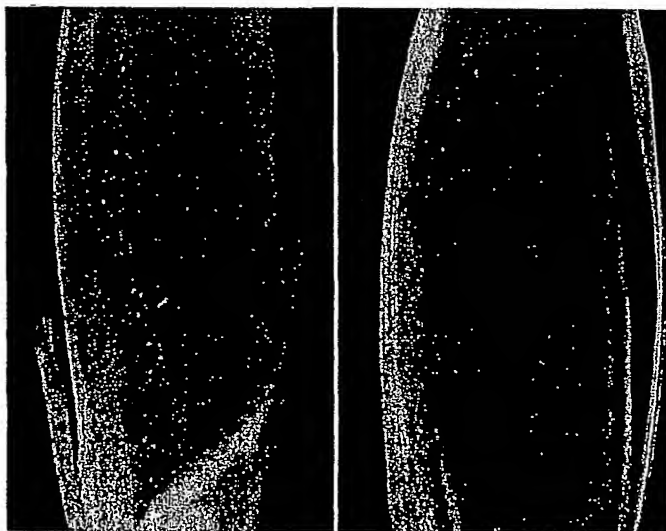
A



Decoy



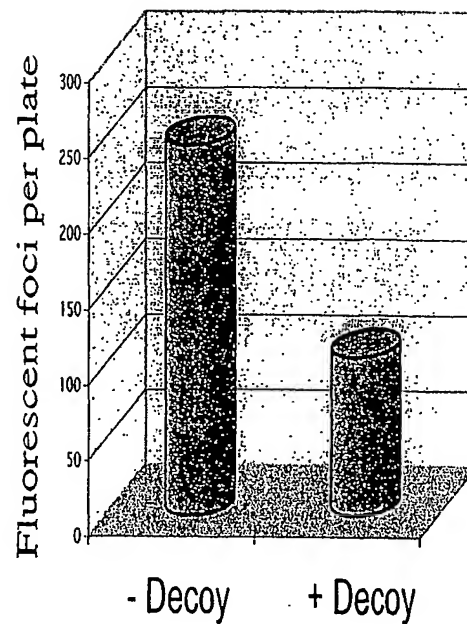
B



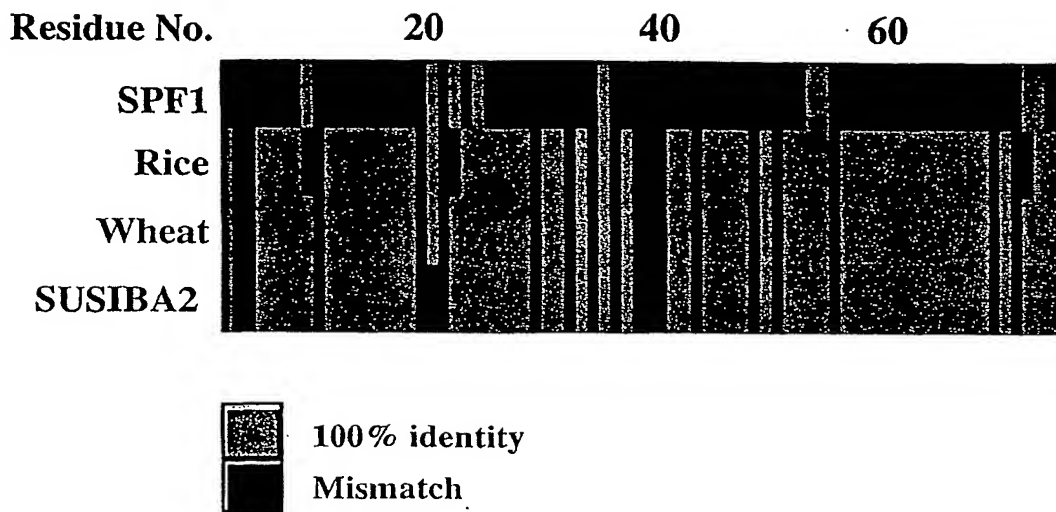
- Decoy

+ Decoy

C



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Figure 11**A****B**

SUSIBA2 MSPARLPISRESCLTIPAGFSPSALLSPVLLTNFKVEPSPTTGLMAAILHKSAHPDM
Rice MSPARLPISREPCLTIPAGFSPSALLESPVLLTNFKVEPSPTTGLMAAILNKSANPDI

SUSIBA2 LPSPRDKSVRNAHEDRGSRDFEFKPHLNSSSSQSLAPAMSDLKKHEHSMONOSYNPSSSSS
Rice LPSPRDKUSGSTHEDCGSRDFEFKPHLNSSSSQSLASAINDPKKHEHSMKNESINTALSSD

SUSIBA2 NMVNEENRPFCSRESLLTVNUS-AQNQPVGMVGLTDSMPAEVGTSEPCQMNSSDNAMQEPQ
Rice DMVIDNIPLCSRESLLAVNTESSAPSQLVGMVGLTDSMPAEVGTSELHOMNSSGNAMQESQ

SUSIBA2 SENVALKSADDGYNWRKYGQKHVKGSNPRSYKCTHPNCEVKKLLERAVDGLITEVVYK
Rice PESVAEKSAEDGYNWRKYGQKHVKGSNPRSYKCTHPNCDVKKLLERSIDGOITEVVYK
=====

SUSIBA2 GRHNHPKPOPNNRLAGGAVPSNOGGERYDGCASAAADKSSNALSNLANPVHSPGMVEPVPA
Rice GRHNHPKPOPNNRLSAGAVPPIOGGERYDGVATDDKSSNVLSILGNVHTAGMTPEVPA
=====

SUSIBA2 SVSDDDDIDAGGGRPYPGDDATEEEDLESKRKRMESAGIDAALMGKPNREPRVVVQTVSEV
Rice SASDDDDNDAGGGRPYPGDDAVEDDLESKRKRMESAGIDAALMGKPNREPRVVVQTVSEV
=====

SUSIBA2 DILDDGYRWRKYGQKVVGKNPNPRSYKCTSTGCPVRKHVERASHDPKSVITTYEGKHH
Rice DILDDGYRWRKYGQKVVGKNPNPRSYKCTNTGCPVRKHVERASHDPKSVITTYEGKHH
=====

SUSIBA2 EVPAARNATHEMSAPPMKPVVHINSNMPSSTGGMRACEARNETNOYSQAAEDTISLD
Rice EVPASRNATHEMSAPPMKPVVHPINSNMGG-LGGMRACEPRTEPNQYSQAAESDTISLD
=====

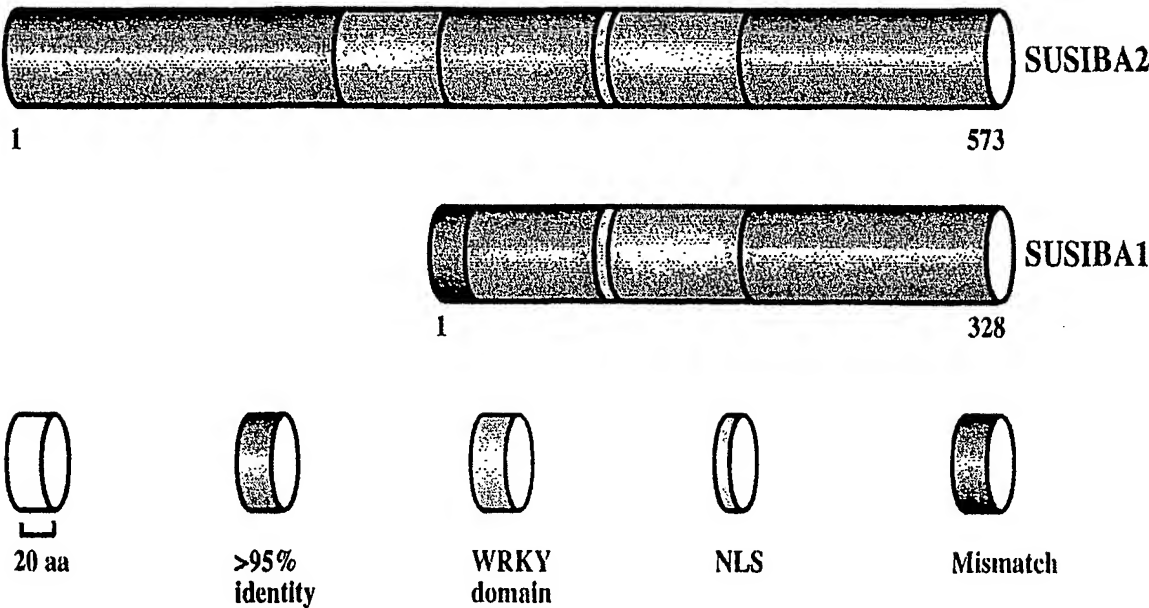
SUSIBA2 LGVGISPNHSDATNQLOSSGPDQMOMQOMGSMYGNMRHPSSMAAPAVQGNNAARVYGS
Rice LGVGISPNHSDATNQLOSSVSDQMOMQOMGSMYSNMGIP-AMAMPTVAGNAASNLVYGS

SUSIBA2 REEKGNEGFTFRATPMDHSANLCYSAGNLVMGP
Rice REEKPSGFTFRATPMDHSANLCYSAGNLVMGP

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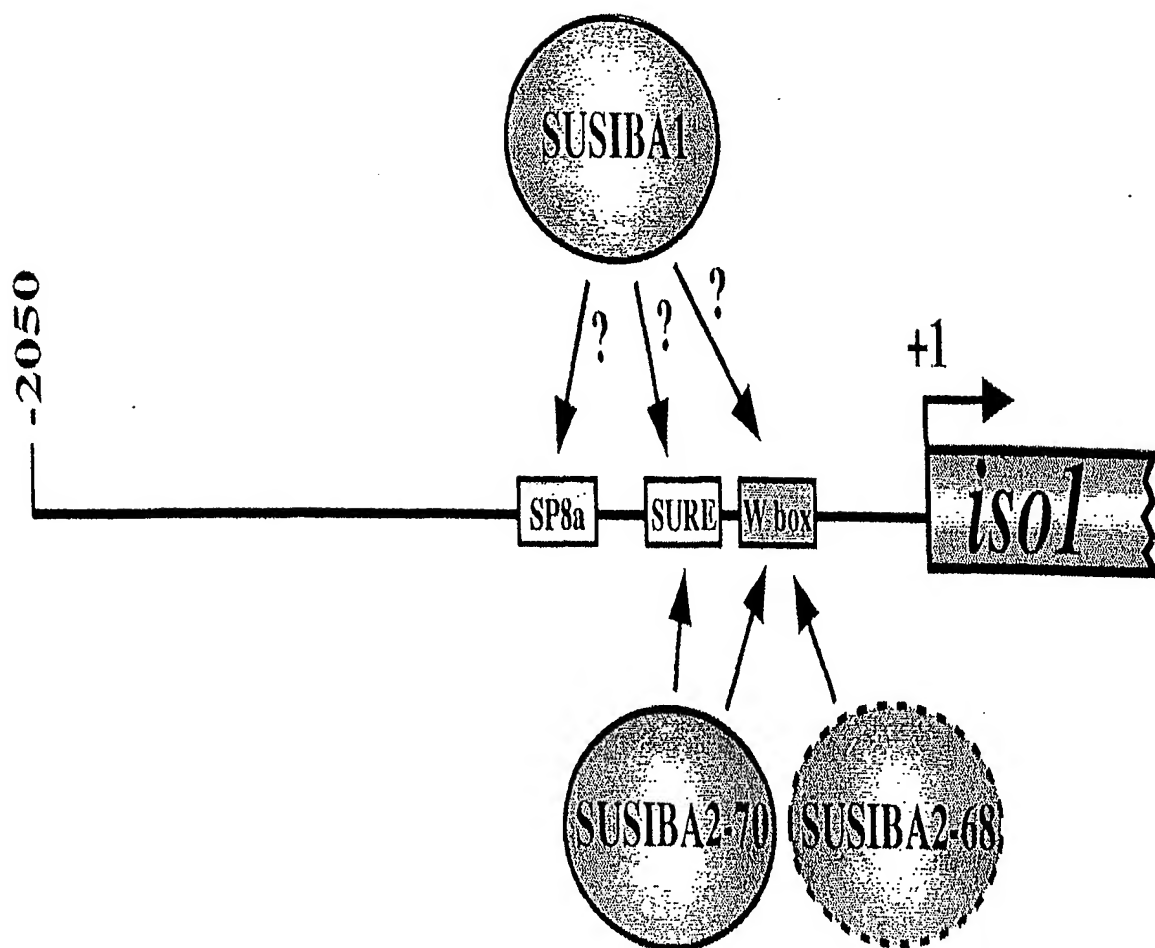
Figure 12



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Figure 13



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Figure 14

SURE-c	-514	-----AAAAAATAAAAGAAATGAAATC-----	-494
SURE-b	-568	-----AATACCAAAAAATAA-TAATAAAA-----	-546
SURE-a	-603	-----CCGAAAAAACTAAGAAAGACCGATG	-578
<i>sbeIIb</i>	-253	-----G-TAATAAAAAA---GG-----G	-240
<i>ssI</i>	-589	-----AAATCCTAAAAAATAAT-----	-570
<i>agpaseS</i>	-1132	-----TA-AAATAAAAC-AAAG-----G	-1116
<i>amy</i>	-1375	-----GCAGAAGATAAAAAAACAA-----	-1356
<i>sbeI</i>	-314	-----ACATA-AAATAAAAAA---AG-----G	-297
<i>sus4</i>	-1287	-----AAAAAGAGTAGAAAAA-----	-1270
<i>vsp</i>	-759	-----AAAGA-AAATAAAAAATAAG-----	-778
PI-II	-548	ATGATAATTA-TTATAAAAAACAAGCAAGT-----	-520
ps20	-172	-----AATACTAATAAAGAA-TAGAAAAA-----G	-149

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